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AC O70410;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative pheromone receptor V2R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RC MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RC Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053986; AAC08413.1; -
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DFBFA48D CRC64;
Query Match 65.0%; Score 740; DB 2; Length 912;
Best Local Similarity 69.7%; Pred. No. 4.3e-61;
Matches 145; Conservative 25; Mismatches 30; Indels 8; Gaps 2;
QY 17 FLAFLWALGSEAKKEEERTCRLLGK-----CVDAAHSLVIGLFPIDSRTPANES 71
Db 12 FLAFLWALGVA--QNKTEEVQCRLMKAKENLGVDAKNSLVIAGLFPHSRLLPVDEA 68
QY 72 ILEPASAKCEGFNFRFWKAMHMIKEINKRKDILPNITLGYQIPDFCFTISKSVREAV 131
Db 69 ILEPSPMCEGFNFRGFRWKMTHIETKEINERKDLIPNHTLGYQIPDFCFTISKAMESS 128
QY 132 LVFLTQGEENRPNRPNSTGTAPAGIVGAGGSFLSVPASRTILGYLYLPQVGYTSTCVILSD 191
Db 129 LVFLTQGEQKFNPNRSTGTSLAALVSGSGSSLSVAASRLILGYLYPQVGYTSSCSILSD 188
QY 192 KYQPPSYLRVLTADSKIQSKAVKRIQHF 219
Db 189 KFQPPSYLRVLPDNLQSEAVNLKHF 216
RESULT 3
QSC0M6 PRELIMINARY; PRT; 476 AA.
ID QSC0M6
AC QSC0M6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933425M15 product:similar to PUTATIVE PHEROMONE
DE RECEPTOR V2R2, full insert sequence.
GN Name=4933425M15R1K;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (KISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RC Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RC Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RC Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RC Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RC Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RC Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RC Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RC Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RC Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RC Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK030224; BAC26854.1; -
DR HSSP; P23385; LEWK.
DR MGD; MGI:2441693; 4933425M15R1K.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00592; CASENSINGR.

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DR PRINTS; PR00248; GPCRNGR.
KW Receptor.
SQ SEQUENCE 476 AA; 54264 MW; 75AA125B45A4BAP CRC64;

Query Match 53.9%; Score 613; DB 2; Length 476;
Best Local Similarity 58.7%; Pred. NO. 2.1e-49;
Matches 122; Conservative 31; Mismatches 49; Indels 6; Gaps 2;

QY 17 FLAFLWAEIGSGSAKEBEKERTCRLLGK-----CVDAENHSLVIGLFPIDSRTPANES 71
DB 14 FTVFLWVLYTQ-YPHIDQNVICRLLRKFNLCGYVEAHNSVVIGLFPVHYRTWPTSDS 72

QY 72 ILEPASAKCEGNGFQFRWKKAMHMKINRKRKIDLPNITLGYQIFDTCFTISKSVEAV 131
DB 73 DBEIESPMCEGNGFNGFRWKKMTIHTIKENRKRKIDLPNHTLGYQIFDNCFSITKAMES 132

QY 132 LVPFLTQGEENRPNRSTGAPAGIVGAGSFLSPASRILGLYLPQVGYTSTCVILSD 191
DB 133 SVFLTQGEYKPNRSTGKFLIGIAGGSTMSAAVSRVGIHVPQGVYASSSSIFSN 192

QY 192 KYQPPSYLRVIASDKIQSKAVVKRIQHP 219
DB 193 DIQPPYLITPSDKQSEAINVLIHFP 220

RESULT 4
Q8C0V4 PRELIMINARY; PRT; 618 AA.
AC Q8C0V4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930518C23 product:weakly similar to PUTATIVE PHEROMONE
DE RECEPTOR V2R2, full insert sequence.
GN Names=4930518C23Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029734; BAC36588.1; -
DR MGD; MGI:2441682; 4930518C23Rik.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004930; P:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca sens receptor.
DR InterPro; IPR000337; GPCR_Mg2.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRNGR.
KW Receptor.
SQ SEQUENCE 618 AA; 69142 MW; 240B395BACCD5424 CRC64;

Query Match 48.1%; Score 547; DB 2; Length 618;
Best Local Similarity 66.0%; Pred. No. 5.4e-43;
Matches 103; Conservative 22; Mismatches 31; Indels 0; Gaps 0;

QY 64 RTPANESILEPASAKCEGNGFQFRWKKAMHMKINRKRKIDLPNITLGYQIFDTCFT 123
DB 19 RTMPTSDSDEIESPMCEGNGFNGFRWKKMTIHTIKENRKRKIDLPNHTLGYQIFDTCFS 78

QY 124 ISKSVEAVLVLVTQGEENRPNRSTGAPAGIVGAGSFLSPASRILGLYLPQVGYT 183
DB 79 VSKAMETAWTLTQGEKKPNRSTGKVLGIIGSSSLSVTARIFGLYMPQVGYT 138

QY 184 STCVILSDKYQPPSYLRVIASDKIQSKAVVKRIQHP 219
DB 139 SSSAILSDKFPQPPSPVRSIPSDKIQIEAMVTLIHF 174

RESULT 5
O73635 PRELIMINARY; PRT; 940 AA.
AC O73635;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Calcium2+ sensing receptor.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
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Dd 92 TLGRIYRFDTCNTVSKALEATLSFVAQNKIDSLNDFPCNCETHDHPSTPIAVVGASGSAAVT 151

Qy 167 PASRIILGLYLPOGVGTSTCVILSDKYOFFPSYLRLVIASDKIQSAVVVKRIQH F 219
 : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 152 AVANLLGLFYFIQISVASSRLLSNKNQFKSFMRTIPTDEHQATAMADIIFY 204

RESULT 8

Q6XAFI PRELIMINARY; PRT; 941 AA.

ID Q6XAF1 AC Q6XAF1;
DT 05-JUL-2004 (TrEMBLrel_27, Created)
DT 05-JUL-2004 (TrEMBLrel_27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel_27, Last annotation update)
DE Calcium polyvalent cation receptor 1.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxId=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=kidney;

RA Nearing J.A., Harris W.;
RL Submitted (PEB-2003) to the EMBL/GenBank/DDBJ databases.
DR ENBL; AY245445; AAP79925.1; .
DR GO; GO:0016020; C:membrane; IEA.
DR CO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . ; IEA.
DR GO; GO:0004872; R:receptor activity; IEA.
DR DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRMRGR.
DR PROSITE; PS00979; G_PROTEIN_REC EP_F3_1; 1.
DR PROSITE; PSS0259; G_PROTEIN_REC EP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 941 AA; 106130 MW; 06119219CDF62DIF CRC64;

Query Match 31.1%; Score 354; DB 2; Length 941;
Best Local Similarity 41.6%; Pred.No.1.9e-24;
Matches 72; Conservative 38; Mismatches 57; Indels 6; Gaps 3

Qy 53 LVIGLGFPPIDSRTIPANESI-IEPASAKCEGFNFQRFRWKKAMTHMKIKNGKDILPNI 111
 :::||| ::||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 32 ILLEGFLPFMHFGVTSKDQAARPESTECVRYNFRGWLRQAMTFAIEEINNSSLTPNI 91

Qy 112 TLGYQLFDCTFTISKVEALVFELQGQE--ENRFNPFSNGAPPA--GIIVGGSGSFSLV 166
 ||||| FDCT FT ISKV EAL VF EL QGE --EN RF NP FS NG AP PA --GI IV GG SG SF SL V
Db 92 TLGRIYRFDTCNTVSKALEATLSFVAQNKIDSLNDFPCNCETHDHPSTPIAVVGASGSAAVT 151

Qy 167 PASRIILGLYLPOGVGTSTCVILSDKYOFFPSYLRLVIASDKIQSAVVVKRIQH F 219
 : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 152 AVANLLGLFYFIQISVASSRLLSNKNQFKSFMRTIPTDEHQATAMADIIFY 204

RESULT 9

Q6XAF3 PRELIMINARY; PRT; 941 AA.

ID Q6XAF3 AC Q6XAF3;
DT 05-JUL-2004 (TrEMBLrel_27, Created)
DT 05-JUL-2004 (TrEMBLrel_27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel_27, Last annotation update)
DE Calcium polyvalent cation receptor 2.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI TaxId=8030;

DR	Pfam, PF07562; NCD3G; 1.
DR	PRINTS; PR00592; CASENSINGR.
DR	PRINTS; PR00248; GPCRMR.
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR	PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR	PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
KW	Receptor.
SQ	SEQUENCE 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;
	Query Match 31.0%; Score 353; DB 2; Length 1027;
	Best Local Similarity 41.6%; Pred. No. 2.6e-24;
	Matches 72; Conservative 39; Mismatches 56; Indels 6; Gaps 3;
QY	53 LVIGGLFPIDSRITPANESI-LBPASAKCEGFNFQRFMKAMHMIKEINKRKDIILPNI 111
DB	36 IILGLGLFIFGVAAKDQLKSPEATKCIRYNFRGRFLQAMIFAIEINNMTFLPNI 95
QY	112 TLGYQIPIFTCTISKSVEAVLFLTGE---ENRNPNFRNSTGAPFA--GIIVGAGGSLSV 166
DB	96 TLGYRIPIFTCNVSKALENTLSFVAQNKTDSLMLDEFNCSDHIPSTTIAVGATGGSGIST 155
QY	167 PASRLILGYLYLPQVGYTSTCVLLSDKYQPSPYLRLVIASDKIOASKAVVRKIHF 219
DB	156 AVANLLGLFYIPQVSAYSSRRLLSNKNYKAFLRTIPNDDEQATAWAIIHF 208
RESULT 11	
CASR_HUMAN	
ID	CASR HUMAN STANDARD; PRT; 1078 AA.
AC	P41180; Q13912; Q16108; Q16109; Q16110; Q16379;
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
DE	Cell calcium-sensing receptor).
GN	Name=CaSR; Synonyms=GPRC2A, PCAR1;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI	TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Pearce S.H.S.; Thakker R.V.;
RL	Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Parathyroid;
RX	MEDLINE=95279439; PubMed=7759551; DOI=10.1074/jbc.270.21.12919;
RA	Garrett J.E., Capuano I.V., Hammerland L.G., Hung B.C., Brown B.M.,
RA	Hebert S.C., Nemeth E.F., Fuller F.;
RT	"Molecular cloning and functional expression of human parathyroid
RT	calcium receptor cDNAs.";
RL	J. Biol. Chem. 270:12919-12925(1995).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RX	MEDLINE=95408281; PubMed=7677761;
RA	Aida K., Koishi S., Tawata M., Onaya T.;
RT	"Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
RT	human kidney.";
RL	Biochem. Biophys. Res. Commun. 214:524-529(1995).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96343808; PubMed=8756555; DOI=10.1210/en.137.9.3842;
RA	Fretschel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi V.,
RA	Raupe F.;
RT	"Expression of a calcium-sensing receptor in a human medullary thyroid
RT	carcinoma cell line and its contribution to calcitonin secretion.";
RL	Endocrinology 137:3842-3848(1996).
RN	[5]
RP	SEQUENCE OF 643-908 FROM N.A.
RX	MEDLINE=96193893; PubMed=8613532;

RA Nakayama T., Minato M., Nakagawa M., Soma M., Tobe H., Aoi N.,
RA Kosuge K., Sato M., Ozawa Y., Kamatsuse K., Kokubun S.;
RT "A novel mutation in Ca2+-sensing receptor gene in familial
RL hypocalcemic hypercalcemia.";
RL Endocrine 15:277-282(2001).
CC -I- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=P41180-1; Sequence=Displayed;
CC
CC IsoId=P41180-2; Sequence=VSP_002035;
CC -I- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
CC liver, heart, skeletal muscle, or placenta.
CC -I- DISEASE: Defects in CASR are the cause of familial hypocalcemic
CC hypercalcemia, type 1 (FHH) [MIM:145980]; in which the receptor
CC has reduced activity. FHH is characterized by altered calcium
CC homeostasis. Affected individuals exhibit mild or modest
CC hypercalcemia, relative hypocalciuria, and inappropriately normal
CC PTH levels.
CC -I- DISEASE: Defects in CASR are the cause of neonatal severe primary
CC hyperparathyroidism (NSHPT) [MIM:239200]; in which the receptor
CC has reduced activity. NSHPT is a rare autosomal recessive life-
CC threatening disorder characterized by very high serum calcium
CC concentrations, skeletal demineralization, and parathyroid
CC hyperplasia. In some instances NSHPT has been demonstrated to be
CC the homozygous form of FHH.
CC -I- DISEASE: Defects in CASR are the cause of autosomal dominant
CC hypocalcemia (ADH) [MIM:601198]; in which the receptor is
CC activated at subnormal Ca(2+) levels.
CC -I- DISEASE: Defects in CASR are the cause of autosomal dominant
CC hypoparathyroidism (FHH) [MIM:146200]. FHH is characterized by
CC hypocalcemia and hyperphosphatemia due to inadequate secretion of
CC parathyroid hormone. Symptoms are seizures, tetany and cramps.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
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CC EMBL; X81086; CAA56990.1; -;
CC EMBL; U20759; AAA86503.1; -;
CC EMBL; U20760; AAA86504.1; -;
CC EMBL; D50855; BAA09453.1; -;
CC EMBL; S83176; AAB46873.1; -;
CC EMBL; S79217; AAB35262.2; -;
CC EMBL; S68032; AAB29413.2; ALT_SEQ.
CC EMBL; S68033; AAB29414.1; -;
CC EMBL; S68036; AAB29415.1; -;
CC EMBL; S81755; AAD14370.1; -;
CC HSSP; P23385; LEWK.
CC Genes; HGNC:1514; CASR.
CC MIM; 601199; -;
CC MIM; 145980; -;
CC MIM; 239200; -;
CC MIM; 601198; -;
CC MIM; 146200; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.
CC GO; GO:0006874; P:calcium ion homeostasis; TAS.
CC GO; GO:0005513; P:calcium ion sensing; TAS.
CC GO; GO:0007635; P:chemosensory behavior; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
CC GO; GO:0009653; P:morphogenesis; TAS.

DR GO; GO:0001503; P:ossification; TAS.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR00068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00379; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00380; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00380; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
Query Match 31.0%; Score 353; DB 1; Length 1078;
Best Local Similarity 37.1%; Pred. No. 2.8e-24;
Matches 78; Conservative 44; Mismatches 64; Indels 24; Gaps 5;
QY 18 LAFLW--AELGSEAKKEEERTCLLGLKCVDAENHSLVIGLFLPDSRTIPANESI-LR 74
DB 11 LALTWHTSAYGPDQRAQKGD-----IILGLFPFHFGVAAKQDLKSR 54
QY 75 PASAKCEGFNFQFRMKAMIMIKENRKRDKILPNITLGYQIFDFTTISKSVAVLVF 134
DB 55 PESVECIYRFRGFRWLQAMIFAEINSSPALLPNLTGLYRIFDTCNTVSKALEATLSF 114
QY 135 LTGQE---ENRNFNSTGAPPA--GIYVAGSGPSLVPASRILGLYLLPQVGYTSTCVIL 189
DB 115 VAQNKIDSLNLDFFCNSEHPIETIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLL 174
QY 190 SDKYOPPSYLRVIASDKIQSKAVVKRIQHP 219
DB 175 SNKNQFKSLRTIPNDEHQTAMADIIIEYF 204
RESULT 12
Q80ZAB PRELIMINARY; PRT; 1079 AA.
ID Q80ZAB
AC Q80ZAB; 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Calcium sensing receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Dorsal root ganglion;
RA Eukotki R., Bian K., Wang Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214122; AAO59490.1; -;
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR00068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF01562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00379; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00380; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00529; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 1079 AA; 120830 MW; 50A2D026AE65CEB1 CRC64;
Query Match 31.0%; Score 353; DB 2; Length 1079;
Best Local Similarity 36.7%; Pred. No. 2.8e-24;
Matches 77; Conservative 45; Mismatches 64; Indels 24; Gaps 5;


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FT CONFLICT 45 45 /FTID=VSP 002036.
FT CONFLICT 304 304 A -> S (in Ref. 2).
FT CONFLICT 410 410 L -> P (in Ref. 3).
FT CONFLICT 566 566 G -> D (in Ref. 2 and 3).
FT CONFLICT 595 595 V -> A (in Ref. 2).
FT CONFLICT 610 610 Y -> H (in Ref. 2, 3 and 5).
FT CONFLICT 814 814 E -> V (in Ref. 5).
FT CONFLICT 889 889 F -> L (in Ref. 2).
FT CONFLICT 906 909 TGSN -> SGWI (in Ref. 2).
FT CONFLICT 1057 1057 V -> M (in Ref. 2).
FT CONFLICT 1064 1064 V -> A (in Ref. 2).
FT CONFLICT 1076 1076 I -> V (in Ref. 2).
SQ SEQUENCE 1079 AA; 120839 MW; AAF8D8D472736D6E CRC64;

Query Match 30.9%; Score 352; DB 1; Length 1079;
Best Local Similarity 37.1%; Pred. No. 3.4e-24;
Matches 78; Conservative 44; Mismatches 64; Indels 24; Gaps 5;

QY 18 LALFW--ABLSGSAKEEKEERTCLLGGKVDNHSVLVIGGLFPIDSRTPANESI-LE 74
DB 11 LALWSSAYGPDQAQKGD-----IILGGLFPIHFVAAKDQDKSR 54
QY 75 PASAKCEGFNFORFRWKAMHIMIKRDKILPNITLGYQIFDTCFTISKSVEAVLVP 134
DB 55 PESVECIYRNFGRFWLQAMIFAEINSSPALLPNMTLGYRIFDTCNTVSKALEATLSF 114
QY 135 LTQGE---ENRPNFRNSTGAPPA--GIVGAGSFLSVPASRIILGYLPLQVGYTSCVIL 189
DB 115 VAQNKIDSLNLDKFCNCSHEIPSTIAVVGATGVSTAVANLLGLFYIPQVYASSRLL 174
QY 190 SDKYQPPSVLRVIASDKIOSKAVVKRIQHP 219
DB 175 SNKNQPKSFLRTPNDEHQATAMADIIIEYF 204

RESULT 14
CASR-RAT STANDARD; PRT; 1079 AA.
AC P48442;
DT 01-FEB-1996 (Rel. 33, Created)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (CasR) (Parathyroid
DE Cell calcium-sensing receptor).
GN Name=Casr; Synonyms=Gprc2a, Pcarl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney outer medulla;
RX MEDLINE=95116508; PubMed=7724534;
RA Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.;
RT "Cloning and functional expression of a rat kidney extracellular
RT calcium/polyvalent cation-sensing receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
RN [2]
RP SEQUENCE OF 1-294 FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95241465; PubMed=7724534;
RA Ruat M., Snowman A.M., Snyder S.H.;
RT "Calcium sensing receptor: molecular cloning in rat and localization
RT to nerve terminals.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
CC -1- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.

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CC -----
DR EMBL; U10354; AAC52149.1; -.
DR EMBL; U20289; AAC52195.1; -.
DR PIR; I59362; I59362.
DR HSP; P23385; IEWK.
DR RGD; 2277; Caer.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR00068; Ca_sens receptor.
DR InterPro; IPR00337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
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RESULT 15

CASR_BOVIN

ID -CASR_BOVIN STANDARD; PRT; 1085 AA.

AC P35384;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 23-OCT-2004 (Rel. 45, Last annotation update)

DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Cell calcium-sensing receptor).

DE Names-CASR; Synonyms=gPCR2A, pCAR1;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

[1]

RN SEQUENCE FROM N.A.

RP TSSUE=Parathyroid;

RC MEDLINE=94077182; PubMed=8255296; DOI=10.1038/366575a0;

RA Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O., Sun A., Hediger M.A., Lytton J., Hebert S.C.;

RT "Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid.";

RL Nature 366:575-580(1993).

CC -1- FUNCTION: Senses changes in the extracellular concentration of calcium ions. The activity of this receptor is mediated by a G-protein that activates a phosphatidylinositol-calcium second messenger system.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.

CC -----

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CC -----

DR EMBL; S67307; AAB29171.1; --

DR PIR; S40476; S40476.

DR HSP; P23385; 1EWT.

DR InterPro; IPR001828; ANF_receptor.

DR InterPro; IPR000068; Ca_sens_receptor.

DR InterPro; IPR000337; GPCR_Mgr.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

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KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 1085 Extracellular calcium-sensing receptor.

FT DOMAIN 20 613 Extracellular (Potential).

FT TRANSMEM 614 636 1 (Potential).

FT DOMAIN 637 650 Cytoplasmic (Potential).

FT TRANSMEM 651 671 2 (Potential).

FT DOMAIN 672 682 Extracellular (Potential).

FT TRANSMEM 683 701 3 (Potential).

FT DOMAIN 702 725 Cytoplasmic (Potential).

FT TRANSMEM 726 746 4 (Potential).

FT DOMAIN 747 770 Extracellular (Potential).

FT TRANSMEM 771 793 5 (Potential).

FT DOMAIN 794 809 Cytoplasmic (Potential).

FT TRANSMEM 807 826 6 (Potential).

FT DOMAIN 830 837 Extracellular (Potential).

FT TRANSMEM 838 863 7 (Potential).

FT DOMAIN 864 1085 Cytoplasmic (Potential).

FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).

FT CATABOL 131 131 N-linked (GlcNAc...) (Potential).